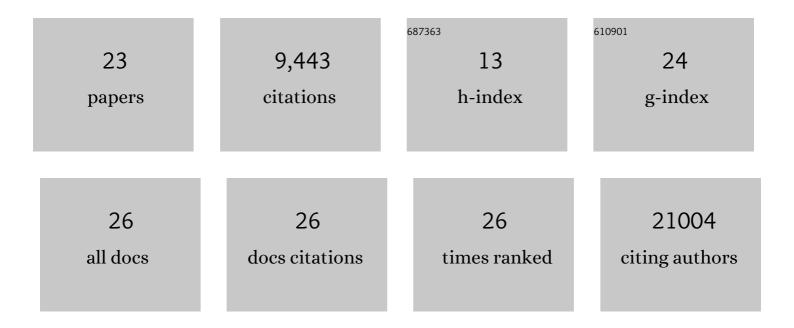
Jaap Heringa

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	PIPENN: protein interface prediction from sequence with an ensemble of neural nets. Bioinformatics, 2022, 38, 2111-2118.	4.1	10
2	A framework for exhaustive modelling of genetic interaction patterns using Petri nets. Bioinformatics, 2020, 36, 2142-2149.	4.1	3
3	FAIR Principles: Interpretations and Implementation Considerations. Data Intelligence, 2020, 2, 10-29.	1.5	149
4	Tailor-made multiple sequence alignments using the PRALINE 2 alignment toolkit. Bioinformatics, 2019, 35, 5315-5317.	4.1	4
5	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	16.3	69
6	The potential use of big data in oncology. Oral Oncology, 2019, 98, 8-12.	1.5	40
7	SeRenDIP: SEquential REmasteriNg to Derlve profiles for fast and accurate predictions of PPI interface positions. Bioinformatics, 2019, 35, 4794-4796.	4.1	21
8	Bioinformatics in the Netherlands: the value of a nationwide community. Briefings in Bioinformatics, 2019, 20, 375-383.	6.5	15
9	Motif-Aware PRALINE: Improving the alignment of motif regions. PLoS Computational Biology, 2018, 14, e1006547.	3.2	7
10	Training for translation between disciplines: a philosophy for life and data sciences curricula. Bioinformatics, 2018, 34, i4-i12.	4.1	5
11	Aurora kinase A (AURKA) interaction with Wnt and Ras-MAPK signalling pathways in colorectal cancer. Scientific Reports, 2018, 8, 7522.	3.3	38
12	Seeing the trees through the forest: sequence-based homo- and heteromeric protein-protein interaction sites prediction using random forest. Bioinformatics, 2017, 33, 1479-1487.	4.1	66
13	Both Intrinsic Substrate Preference and Network Context Contribute to Substrate Selection of Classical Tyrosine Phosphatases. Journal of Biological Chemistry, 2017, 292, 4942-4952.	3.4	8
14	Bridging the translational innovation gap through good biomarker practice. Nature Reviews Drug Discovery, 2017, 16, 587-588.	46.4	48
15	Systematically linking tranSMART, Galaxy and EGA for reusing human translational research data. F1000Research, 2017, 6, 1488.	1.6	8
16	Construction and Experimental Validation of a Petri Net Model of Wnt/β-Catenin Signaling. PLoS ONE, 2016, 11, e0155743.	2.5	16
17	The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 2016, 3, 160018.	5.3	8,670
18	Integration of EGA secure data access into Galaxy. F1000Research, 2016, 5, 2841.	1.6	7

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#	Article	IF	CITATIONS
19	Sequence specificity between interacting and non-interacting homologs identifies interface residues – a homodimer and monomer use case. BMC Bioinformatics, 2015, 16, 325.	2.6	18
20	Multi-Harmony: detecting functional specificity from sequence alignment. Nucleic Acids Research, 2010, 38, W35-W40.	14.5	51
21	Multi-RELIEF: a method to recognize specificity determining residues from multiple sequence alignments using a Machine-Learning approach for feature weighting. Bioinformatics, 2008, 24, 18-25.	4.1	83
22	Sequence harmony: detecting functional specificity from alignments. Nucleic Acids Research, 2007, 35, W495-W498.	14.5	34
23	Sequence comparison by sequence harmony identifies subtype-specific functional sites. Nucleic Acids Research, 2006, 34, 6540-6548.	14.5	64